AMENDMENTS TO THE CLAIMS

1.-4. (Canceled)

5. (Original) A method of identifying whether a protein is susceptible to forming amyloid, the method comprising analyzing the amino acid sequence of the protein to determine whether the protein contains a predicted discordant helix, wherein the presence of predicted discordant helix is an indication that the protein is susceptible to forming amyloid.

6. (Original) The method of claim 5, wherein the discordant helix is at least six amino acids in length.

7. (Original) A method of decreasing the rate of formation of β-strand structures between at least two discordant helix-containing polypeptides, the method comprising contacting the discordant helix-containing polypeptides with a compound that stabilizes an α-helical form of the discordant helix.

8. (Original) A method of treating an individual having or at risk for an amyloidosis, the method comprising administering to the individual a therapeutically effective amount of a compound that stabilizes an α-helical form of a discordant helix-containing polypeptide that forms amyloid.

9. (Original) The method of claim 8, wherein the amyloidosis is selected from the group consisting of prion diseases and Alzheimer's disease.

10. (New) A method of identifying whether a protein is susceptible to forming amyloid, the method comprising

a. providing the amino acid sequence of a protein;

b. identifying amino acids in the protein that are experimentally determined to form α-helix or are predicted to form α-helix;

c. identifying amino acids in the protein that are experimentally determined to form β-structure or are predicted to form β structure;

d. determining experimentally whether there is overlap between the amino acids of (b) and the amino acids of (c); wherein the presence of overlap between the amino acids experimentally determined to form α-helix and predicted to form β-structure indicates that the protein is susceptible to forming amyloid.

11. (New) The method of claim 10, wherein the identification of amino acids is performed using PHD analysis.

12. (New) The method of claim 10, wherein the identification of amino acids is performed using PHD analysis and Chou-Fassman analysis and the identified amino acids are the same using both methods.

13. (New) The method of claim 10, wherein the discordant helix is at least 12 amino acids in length.